

CLAIMS

I claim:

1. A method for screening for a transdominant intracellular bioactive agent capable of altering the phenotype of a cell, said method comprising the steps:
- 5 a) introducing a molecular library of randomized candidate nucleic acids into a plurality of cells, wherein each of said nucleic acids comprises a different nucleotide sequence;
- b) screening said plurality of cells for a cell exhibiting an altered phenotype, wherein said altered phenotype is due to the presence of a transdominant bioactive agent.
- 10 2. A method according to claim 1 further comprising the step:
- c) isolating said cell exhibiting an altered phenotype.
3. A method according to claim 2 further comprising the step:
- d) isolating a candidate nucleic acid from said cell.
- 15 4. A method according to claim 2 or 3 further comprising the step:
- e) isolating a target molecule using
- i) a candidate nucleic acid; or
- ii) the expression product of a candidate nucleic acid.
- 20 5. A method according to claim 1 wherein said randomized candidate nucleic acids are expressed in said cells to produce a plurality of randomized candidate expression products.
6. A method according to claim 5 wherein said randomized candidate expression products are peptides.
7. A method according to claim 5 wherein said randomized candidate expression products are nucleic acid transcripts.
- 25 8. A method according to claim 1 wherein said nucleic acids further comprise a presentation sequence capable of presenting said expression product in a

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conformationally restricted form.

9. A method according to claim 1 wherein said introducing is with retroviral vectors.
10. A method according to claim 1 wherein said cells are mammalian cells.
- 5 11. A method according to claim 1 wherein said library comprises at least 10^4 different nucleic acids.
12. A method according to claim 1 wherein said library comprises at least 10^5 different nucleic acids.
- 10 13. A method according to claim 1 wherein said library comprises at least 10^6 different nucleic acids.
14. A method according to claim 1 wherein said library comprises at least 10^7 different nucleic acids.
- 15 15. A method according to claim 1 wherein said library comprises at least 10^8 different nucleic acids.
16. A molecular library of retroviruses comprising at least 10^4 different randomized nucleic acids.
17. A molecular library of retroviruses according to claim 21 comprising at least 10^5 different randomized nucleic acids.
- 20 18. A molecular library of retroviruses according to claim 21 comprising at least 10^6 different randomized nucleic acids.
19. A molecular library of retroviruses according to claim 21 comprising at least 10^7 different randomized nucleic acids.
20. A molecular library of retroviruses according to claim 21 comprising at least

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